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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Q19791 ceanorhabdi
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Gene 283:49-62(2002).

EMBL; AJ31573; CAC86014.1; -.

Integrin; Protease.
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OBTE58;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metalloprotease disintegrin 15 with thrombospondin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-21856482; PubMed-11867212;
Cal S., Obaya A.J., Llamazares M.,
Lopez Otin C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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   121 GGLRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASGW
                                                                                61
                                                                                                                                                                                                                      949;
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950 AA; 103286 MW;
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Q91256;
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T 01-DEC-2001 (TrEMBLrel. 19, Created)
T 01-DEC-2001 (TrEMBLrel. 20, Last sequence update)
T 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
E Similar to a disintegrin and metalloproteinase with the motifs 1 (ADAMTS-1) (Fragment).

E Mus musculus (Mouse).
E Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euromaniai; Eutheria; Rodentia; Sciurognathi; Muridae; M. NCBI_TaxID-10090;
      SEQUENCE FROM N.A. Strausberg R.; Submitted (JUN-200
                                                                                                                                                                                                                                                                                                901
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Matches 308
Watson A., F

"2.2 Mb of celegans.";

Nature 358:

EMBL: Z6936

EMBL: Z6936

EMBL: Z6936
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Q19791; Q27524;
01-NOV-1996 (TREMBLRE1. 0
01-NOV-1998 (TREMBLRE1. 0
01-DEC-2001 (TREMBLRE1. 1
F25H8.3 protein.
                                                                                        Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Couls
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 M. of contiguous nucleotide sequence from chromosome III o
                                                                                                                                                                                                                                                                                                                          SEQUENCE
Gajadsty
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Q19791;
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Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caen
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                             Submitted (FEB-1996)
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Integrin.
NON_TER 1
SEQUENCE 340 AA; 3:
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 re 368:32-38(1994).;
Z69361; CAA93288.1;
Z69360; CAA93287.1;
Z69361; CAA93287.1;
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Pred. No. 9.5e
L1; Mismatches
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Best Local S
Matches 347
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InterPro; IPR000884; TSP1.
InterPro; IPR000130; AmTpe
Pfam; PF01421; Reprolysin; 1
Pfam; PF00090; tsp_1; 14.
SMART; SM00209; TSP1; 18.
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MEROPS; M12.135;
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                                                                                                             QRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQAS
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GQQSQKLMCLDMSTHRQS------HDRNCQNVLKPKQATRMCNIDCSTRWITEDVSSCS
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                         -----DKSSHPKDPRGPSVLHN----SVLSLSNQVEQPDDRPPARWVAGSWGPCS
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PS50092; TSP1; 6.
PS00142; ZINC_PROTEASE; UNKNOWN_1.
PS00143; ZINC_PROTEASE; UCKNOWN_1.
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TSP1.
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Q8TE60;
Q8TE60;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";

Gene 283:49-62(2002).

EMBL; AJ311903; CAC83612.1; -.

SEQUENCE 1081 AA; 119655 MW; 0438BF645676461E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADAMTS18.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRNYPGYSPSHIPHASQSRETEYHHRRLQKQHFCGRRKKYAP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASGLNDDYVFVTPVEVDSAGSYISHDILHNGRK---KRSAQNARSSLHYRFSAFGQELHL
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                                                                                                                                           MPHDNV-KVCEEVFGKLRANHMMSPTLIQIDRANPWSACSAAIITDFLDSGHGDCLLDQP
                                                                                                                                                                                           DHAILLTGFDICSWKNEPCDTLGFAPTSGMCSKYRSCTINEDTGLGLAFTIAHESGHNEG
                                                                                                                                                                                                                                           DTAILFTRODLCG--ATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFN
                                                                                                                                                                                                                                                                                                                                         LYRHPSILNPINIVVVKVLLLRDRDSGPKVTGNAALTLRNFCAWQKKL-NKVSDKHPEYW
                                                                                                                                                                                                                                                                                                                                                                                           RFDEYGSSGRPRRSAGKSQKGLN----VETLVVADKKMVEKHGKGNVTTYILTVMKVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELKPS-----AILSSHFIVQVLGKDGASETQKPEVQQCFYQGFIRNDSSSSVAVSTCAG
KQAGQYKYPDKLPGQIYDADTQCKWQFGAKAKLCSLGFVKDICKSLWCHRVGHR----
                                           SK--PISLPEDLPGASYTLSQQCELAFGVGSKPCP---YMQYCTKLWC--TGKAKGQMVC
                                                                                             MIHDGEGNPCRKAEG-----NIMSPTLTGNNGVFSWSSCSRQYLKKFLSTPQAGCLVDEP
                                                                                                                                                                                                                                                                                           LFKDGTIGSDINVVVVSLILLEQEPGGLLINHHADQSLNSFCQWQSALIGKNGKRH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSGLIRTRKNEFLISPLPQLLAQEHNYSSPAGHH----PHVLYKRTAEEKIQRYRGYPGS
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Last annotation updat
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Pred. No. 9.2e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local
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Q8TE57;
Q8TE57;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-JUN-2002 (TrEMBLrel. 16 with thrombospondin
                                                                                                                                                                                                                                                                                                                             "Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases with disintegrin and thrombospondin-1 domains."; Gene 283:49-62(2002).
EMBL; AJ315734; CAC86015.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-21856402; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M.,
Lopez-Otin C.;
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                                                                                     QGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSS------DLRRCFY
SGDVNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAPAAQRNSQG---
                                                     ESLHLRLKGPRHDFHMDLRTSSSLVAPGFIVQTL----GKTGTKSVQTLPPEDF--CFY
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                                                                                                                                                                                             Similarity
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1072 AA;
                                                                                                                                                                       Conservative
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                                                                                                                                                                                             24.2%;
                                                                                                                                                                                                                                                                                119491 MW;
                                                                                                                                                                    126;
                                                                                                                                                                 Score 1247.5; DB 4; Length Pred. No. 1.3e-94; 16; Mismatches 386; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                          081EEFF78F47D061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garabaya C.,
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-AHLLQRR
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SHTCGKGWRKRAVACKSTNPSARAQLLPDAVCTSEPKPRMHEACLLQRC
                              SKSCGRGFQRRSLKCVGHG----GRLLARDQCNLHRKPQELDFCVLRPC
                                                                               SASCGSGLQKRAVDC--RGSAGQRTVPA--CDAAHRPVETQAC-GEPC-PTWELSAWSPC
                                                                                                                                                                                                                                                                                                                                                                                         LLDQPSKPI----SLPEDLPGASYTLSQQCELAFGVGSKPCPY---MQYCTKLWC--TGKA
                                                             SRTCGGGAQSRPVQCTRRVHYDSEPVPASLCPQP-APSSRQACNSQSCPPAWSAGPWAEC
                                                                                                                       ECSVSCGGGQMTVREGCYRDLKFQVNMSFCNPKTRPVTGLVPCKVSACPPSWSVGNWSAC
                                                                                                                                                                                   NLIATGPTNETLIVELLFQGR--NPGVAMEYSMPR-----LGTEKQPPAQPSYTWAIVRS
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                                                                                                                                                        VLHNSVLSLSNQVE----QPDDRP----
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Best Local Similarity
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,

Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY094716; AAM11069.1; -. SEQUENCE 1688 AA; 189867 MW; 48FBBDD4DE0CA4D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celniker S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 VEDDPHSMVSVSLCGGMTGYIKTSFGALLIQPVNRTSSDEVLHRVFRKSQRNAR--HAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 FQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNAEPDSFAAVSLCGGLRGAFGYRGAEYVISPLPNASAP-----AAORNSOGAHLLO 158
                   GDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSLLRYSGTGTAVESLQA--SRPILEP
                                                                               CGVCGGDNKSCKKVTG-LFTKPMHGYN------FVVAIPAGASSIDIRQRGYKGLI 720
                                                                                                                            -KDACKLFCRMDMKYTYFMLKSMVTDGTSCAVDSFDKCVNGICRPAGCDNELNSIAKLDK
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                                                                                                                                                                                                                      GKYCEGVRVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVS
                                                                                                                                                                                                                                                    EIYSLDAQCQLSFGNDFGYCPTDEECKRLWCNRTSGNSNEQ--CASSNLPWADGTPCGSS
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                                                               CGVCEGRNDTCHEVTGNLLVSNLLGLNDGNEPNKTLYYVTRIPKGASNIIITQRGYP---
-DONFIVLTDDRDNELLNGKF-LKTYPLKFVYAGVTMQYTGSSSVVEQVNTTYSWKLSRD
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	HDNVKVCEE 379	322 CGATTCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGH	0
	AVEVIRIDE 347	Db 288 RQRPAKLSIGHHGERSLESFCHWQNEEYGGARYLGNNQVPGGKDDPPLVDAAV	8
	AILFTRODL 321	Qy 273 RDRDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTA	ro.
	:: /TKLVLL 28	229 TS-EHTVETLVVADADMVQYHGAEAAQRFILTVMNMVYNMFQHQS	D .
	ILNPINIVVVKVLLL 272	LLTLLATAARLYRHPS	0
	RDWRERRNAIRL 228	Db 182 RKWSLTPSPSAEAQRPEQLCKVLTEKKKPTWGRPSRDWF	0
	RRSGRAKRF 213	VPGGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGE-	o
	EHLIR 181	Db 126 FYSGRVLGHPGSLVSLSACGAAGGLVGLIQLGQEQVLIQPLNNSQGPFSGRE	0
	NSQGAHLLQ 158	DVNAEPDSFAAVSLCGGLRGAFGYRGAEYV-ISPLPN	o
	GRPAELC 125	Db 70 AAPRARPGERALLLHLPAFGRDLYLQLRRDLRELSRGFEVEEAGAARRRG	
	GSSDLRRC 101	STEHLGVPLQGLTO	o
	RRRPRTPP 69	Db 10 LYLPYLLLLVWGLDPGTAYGDAAADVEVYLPWRYRPDDVHLPPLPAAPGPRRRRPRTP	D
	NGRRYYWRGPE 46	RTAGGFEPEREVVVPIRLDPDI	۵
40;	190; Gaps	; Score 1217; DB 4; Length 1 ; Pred. No. 4.7e-92; 138; Mismatches 387; Indels	
		W Integrin; Frotease. SQ SEQUENCE 1095 AA; 121099 MW; A5C6540484754D5D CRC64;	ω >
		DR EMBL, BJ315735; CAC86016.1;	, ט
		disintegrin and thrombospondin-1 domains.";	מט
	ation of with	RT "Cloning, expression analysis, and structural characterization seven novel human ADAMTSs, a family of metalloproteinases	ze ze
		Lopez-Otin C.;	77 7
		MEDLINE = 21856482; PubMed = 11867212;	o 20 ;
		[1]	מט
		<pre>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;</pre>	00
	leostomi;	ens (Human). ; Metazoa; Chordata; Craniata; Vertebrata; Eute	00
		ADAMIS17.	ຄະ
	ns.	01-JUN-2002 (TrEMBLrel. 21, Last amnotation update) Metalloprotease disintegrin 17, with thrombospondin domai	
		L-TUN-2002 (TremBirel 21, Crea	201
		D Q8TE56: PRELIMINARY; PRT; 1095 AA.	≱∺
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		898 ELSAWSPCSKSCGRG	Q.
	CREGCW 1173	b 1122CSAACGELGTREKTYACVQTFTNMQRSNIVDMSYCKLKFDVAYHEECREGC	Ъ
	CGEPCPTW 897	845 AGSWG	Qy
	1121	1076 LPACISTTQGVKVAPQFCDKSAMPKIDDRACNTDCRLNLTVTSISE	ф
	DRPPARWV 844	807	Qy
	LCEGRSHR 1075	1016 LIVQIISLDVSPSKRQDTVLLSYSYTIDKPPDYEAEVEIYRWEMQAPSNCDS	фd
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Q9VF61;
01-MAY-2000;
01-MAY-2000;
01-JUN-2002;
CG6107;
CG6107.
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                         SEQUENCE FROM N.A. STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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13,
21,
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                              Hexapoda; Insecta;
                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                               Brachycera; Muscomorpha;
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    lklos G.L.G.,
Baldwin D.,
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A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mentulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Staden Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Staden Kiamos I., Simpson M., Strong R., Sun E.,

RA Spier E., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Weilliams S.M., Woodage T., Schan M., Zhang G., Zhao Q., Zheng L.,

RA Yel J., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Sheng L.,

RA Kennison D., Weilliams G., Zhao Q., Smith H.O.,

RA Sheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,

RA Sheng X.H., Wang S., Tan M., Wa
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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InterPro; IPR000130; Zn_MTpeptdse
Pfam; PF01562; Pep_M12B_propep; 1
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 2.
SMART; SM00209; TSP1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50215;
PROSITE; PS50092;
PROSITE; PS00142;
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                        326
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                      TCDTLGMADVGTMCDPKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQITAFQEDFYLHLTPDAQFLAPAFSTEHLGVPLQG-----LTGGSSDLRR--CFYSGD
                                                                   L----PHINDQTHSSNEMLKHFCQF---
                                                                                                            LRDRDSGPKV---TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGAT---
                                                                                                                                                                             KFEL--
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                                                                                                                                                                                                                                                                                                                                                                                                                   YNLNVFGRQLHLVLRQDASFV-HNHSMTHIRILKEGEEHPGPETEAEAEQRHLGCFYSGY
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140;
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Pred. No. 4.26
                                                                                                                                                                                                                                          ----GLDDFMSKLEQVQEEEQKSKSRKLNRKKRHYA
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                                                                   · INQSGYER - - - - DTAMLITREPICGSVPGK
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Q9W493;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Lif P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Lif P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVLSEWSTCSKSCGTGSQQREAHCYLHNSR-VSDDLCNPRTKP
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RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA McIntos C., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Zhong X.H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao O., Zheng L., RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Gibbs R.A., Myers E.M., Zhong W., Zhou X., Zhu X., Smith H.O., RA Meroce 287:2185-2195(2000).

DR EMBL; AE003435; AAF46065.1; -.

DR MFDORE M. STAN AND STAN AN
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Best Local
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Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 2.
SMART; SM00209; TSP1; 2.
SMART; SM00209; TSP1; 2.
PR0SITE; PS50021; ADAM_MEPRO; 1.
PR0SITE; PS50021; TSP1; 1.
PR0SITE; PS00142; ZINC_PROTEASE;
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InterPro; IPR001590; I
InterPro; IPR000884;
InterPro; IPR000130;
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RSRRRSGRAKREVSIPRYVETLVVADESMYKEHGADLEHYLLTLLATAARLYRHPSILNP
                                                                                                                                                                                          P--AAQRNS-QGAHLLQRRG--VPGGPSGD--PTSRCGVASGWNPAILRALDPYKPRR--
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                                                                   ETRLEWQARGKVKVQGGRQIRRHHHHHHHHHHHHKKKYRHHQQKISRVPHTKFKYETQFQTE
                                                                                                                                                               PHVVFQRSSVKPKHSLRKRNKRKRGGKSGSGAEVSNCGTR-
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A; 118616 MW;
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DC15455555CB6212 CRC64;
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Q8TE59;
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O1-JUN-2002 (TTEMBLTEL 2
         SEQUENCE FROM N.A.
MEDLINE=21856482; PubMed=11867212;
Cal S., Obaya A.J., Llamazares M.,
                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             1025 VVVADAECGHLQKPAEMEPC 1044
Lopez-Otin C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        762 DSEVQDDRCGVCGGSGDQCQPVRETYTDPFAAKDGAYVEIVTIPARARHILIRE-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        664 GSKKRFDKCGVCGGDNKSCKKVTGLFTKPM----HGYNFVVAIPAGASSIDIRQRGYKGL 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----WRLSNWTACSASCGGGVQHREPICQENGKGESNEPFQRIVSIKRNLLIALGDTLP
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              Llamazares M., Garabaya C.,
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              Quesada V.,
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Q8WXS8;
01-MAR-2002
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
A disintegrin-like and metalloprotease with thrombospondin anotatic 14 precursor
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Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata;
Tharvota; Primates;
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EMBL; AF358656; AAL40229.L; -.
InterPro; IPR002870; Pep_M12B_propep.
InterPro; IPR001590; Reprolysin.
InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Integrin; Protease; Metalloprotease.
Signal 1 22 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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KPEPQIRKCNEQPCQTRWMMTEWTPCSRTCGKGMQSRQVACTQQLSNGTLIRARERDCIG
VGYRQSLSLIERGNPSRSLEQVCRWAHSQQRQDPSHAEHHDHVVFLTRQDF---
                     LRDRDSGPKV-TGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDLCGATTCDTL
                                                                                                                LORRGVP----GGPSGDPTSRCGVASGWNPAILRALDPYKPRRAGFGESRSRRRSGRAKR
                                                                                                                                                                                                                                                                                                         PEDSGDQGLIFQITAFQEDFYLHLTPDAQFLAPAFSTEH-----LGVPLQGLTGGSSD
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                                                                                             Y----SIEVLLVVDDSVVRFHGKEHVQNYVLTLMNIVDEIYHDESLGVHINIALVRLIM
                                                                                                                                                                                        VYRREAVQQEWAEPDGDLHNE-AFGLGDLPNLLGLVGDQ-----LGDTERKRRHAKPGS
                                                                                                                                                                                                                                                                               -QECVYTGGVTGMPGAAVAISNCDGLAGLIRTDSTDFFIEPLERGQ----QEKEASGRTHV
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Pred. No. 4.4e-84;
22; Mismatches 379;
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SEQUENCE FROM N.A.

MEDLINE-21839041; PubMed-11741898;

COllige A., Vandenberghe I., Thiry M., Lambert C.A.

Li S.W., Prockop D.J., Lapiere C.M., Nusgens B.V.;

"Cloning and Characterization of ADAMTS-14, a Nove

Lambert C.A.,

Van

Beeumen

ADAMTS

Displaying ن :

Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;

s (Human). Metazoa; Chordata; C Metazoa; Primates; (

Craniata; Vertebrata; Catarrhini; Hominidae;

Euteleostom1; Homo.

(TrEMBLrel. 21, (TrEMBLrel. 21, (TrEMBLrel. 21,

Last sequence update)
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Created)

Homo sapiens ADAMTS14

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01-JUN-2002
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                                                                                                                                                                                                                                      PAQWRLGAWSQCSATCGEGIQQRQVVCRTNANSLGH-----CEGDR-PDTVQVCSL
                                                                                                                                                                                                                                                          PT-WELSAWSPCSKSCGRGFQRRSLKC-----VGHGGRLLARDQCNLHRKPQELDECVL
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                                                                                                                                                                                                                                                         GDNKSCKKVTGLFTK--PMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNS-QG
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                                                                                     ARWVAGSWGPCSASCGSGLQKRAVDCR---
                                                                                                                                                                              SFILNPKGK---EATSRTFTAMG-LEWEDAVEDAKESLKTSGPLPEAIAILAL-----
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                                                        YEWALKSWAPCSKACGGGIQFTKYGCRRRRDHHMVQRHLCDHKKRPKPIRRRCNQHPCSQ
                                                                                                                                               PRVRYSFYLPKEPREDKSSHPKDPRGPS-----VLHNSVLSL--SNQV--EQPDDRPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QCRFDFGSGYQTCLAFRTFEPCKQLWCS-HPDNPYFCKTKKGPPLDGTECAPGKWCFKGH
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                          -GSAGQRT-----VPACDAAHRPVETQACG----
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"Cloning, expression analysis, and structural characterization seven novel human ADAMTSS, a family of metalloproteinases with disintegrin and thrombospondin-1 domains.";
Gene 283:49-62(2002).
EMBL; AJ345098; CAC87943.1; -
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                 "Structure of von Willebrand Factor-cleaving Protease (ADAMTS13), Metalloprotease Involved in Thrombotic Thrombocytopenic Purpura.", J. Biol. Chem. 276:41059-41063(2001).

EMBL; AY055376; AAL17652.1; -. MEROPS; M12.241; -.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Von Willebrand factor-cleaving protease precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                   Zheng X., Chung D., Takayama T.K., Majerus E.M., Sadler J.E., Fujikawa K.;
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                          PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS50092; TSP1; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                              InterPro; IPR000884; Tsp1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF00090; tsp_1; 4.
                                                                                                                                                                                                 InterPro; IPR001590; Reprolysin. .
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11557746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
     Protease; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             734 KYLLN--GHFVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTP 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   969 PAQWRLGAWSQCSATCGEGIQQRQVVCRTNANSLGH------CEGDR-PDTVQVCSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  849 YEWALKSWAPCSKACGGGIRFTKYGCRRRRDHHMVHRHLCDHKKRPKPIRRRSNQHPCSQ 908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARWVAGSWGPCSASCGSGLQKRAVDCR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCNLEPCPSSASGKSFREEQCEAFNGY-----NHSTNRLTLAVAWVPKYSGVSPRDKCK 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVWVTEEWGACSRSYGKLGVQTRGIQCLLPLSNGTHKVMPAKACAGDRPEARRPCLRVPC
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		·		0 4	PQELDFCVLRPC 95	35 LHRK : 89 AQQP	7 9	p 8
	ARDQCN 934 : ARCRAG 788	RSLKCVGHGGRLL :: RPVRCVEAQGSLLKTLPP	SCGRGFQR : SCGGGLRE	VG :	ETQACG-EPCPT-WE : WPEACVLEPCPPYWA	9 QPE	7 8	β Q
	CDAAH 882 : CQGSQ 728	SAGQRTVPA : QARKELVETVQ	SCGSGLO : : SCGAGLI	AGSWGPC	NQVEQPDDR	26 LSLS 82	ത മ	g Q
	NSV 825	SVGKMTPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSV : :::: EYGNLTRPDITFTYFQPK	RYSFYLE :::: TFTYFQE	SVGKMTPPRV : : EYGNLTRPDI	PILEPLTVEVLSVGKMTPPRVRYSFYLPK : :: : ::: PLQEDADIQVYRRYGEEYGNLTRPDITFTYFQPK	74P 45 IWGP	6 7	d Qy
	ASR 773 EIR 644	QGKYLLNGHFVVSAVERDLVVKGSL-LRYSGTGTAVESLQASR -	-AVERDI	LLNGHFVVS- :: : VVAGKMSISP	GDDNYLALKNS : :: THLAVRIG	17 KGLI : 89 RPLF	5 7	D Qy
	RGY 716 : ANH 588	KPMHGYNEVVAIPAGASSIDIRQRGY : : : : : : : : : : : : :	LFT KI	DNKSCKKVTG	DGNIGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPA 	59 CDGN 32 CDGR	u o	D Qy
-	KAG 658 TFG 531	KCKLICRANGTGYFYYLAPKVVDGTLCSPDST-SVCVQGKCIKAG : :	KVVDGTI : SFLDGTF	IGTGYFYVLAP : GESFIMKRGD	KYSGVSPRDKCKLICRANGTGYFYVLAPKVVDGTLCSP 	05 PKYS 1 75 PHSQ	<u>4</u> 0	p Q
	WV 604 WGAAV 474	TNRLTLAVA	NG : DGQPLRS	KSFREEQCEAFNGYNHS	RVKYRSCNLEPCPSSASGKSFREEQCEAFNG- :	59 RVKY :: 27 DLQA	ı. vı	p Q
	EGV 558 VGA 426	LKGACVERHNLNK-HRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 	CSRTCGG : CSRSCGG	SWAKWDPYGP : RWSSWGPRSP	CVERHNLNK-HRVDG 	00 LKGA 67 SKGR	<u>ო</u> ნ	Дy
	KLC 499 KWC 366	LSQQCELAFGVGSKPCPYMQYCTKLWCTGKAKGQMVCQTRHFPWADGTSCGEGKLC :: : :	WCTGKAK SCHTDPI	MQYCTKL : REHLDMCQAL	SQQCELAFGVGSKPCPY- :: : : : NEQCRVAFGPKAVACTFA	. 7	30 44	da Vo
	SYT 443 : YYS 306	IDRANPWSACSAAIITDELDSGHGDCLLDQPSKPISLPEDLPGASYT	SGHGDCL : : AGRARCV	WSACSAAIITDFLDSGHGDCLLD- : : : WSPC\$RRQLLSLLSAGRARCVWDP	LIQIDRANPWSAC 	3 TLIQ	39 25	ρ δ
	MSP 392 : MAS 251	ADVGTMCDFKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCEEVFGKLRANHMMSP 	AHELGHVFN : AHEIGHSFG	GLPSAFTTAH	ADVGTMCDFKRSCSVIEDDGLPSAFTTAHELGHVFNMPHDNVKVCE	δ ω	33 19	ρ δ δ
	LGM 332 : RGV 195	RDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDL-CGATTCDTLGM 	SDKHPEY : DDTDPGH	CAWQKKLNKV : : CGWSQTINPE	RDSGPKVTGNAALTLRNFCAWQKKLNKVSDKHPEYWDTAILFTRQDL- : : : : : : : PEGAPNITANLTSSLLSVCGWSQTINPEDDTDPGHADLVLYITRFDLE	о 4 ы. п	27 13	B 8
	LLR 273 : ILT 135	VSIPRYVETLVVADESMYKFHGADLEHYLLTLLATAARLYRHPSILNPINIVVVKVLLLR 	LTLLATA LTNLNIG	FHGADLEHYL : AHQEDTERYV	RYVETLVVADESMVK :: :: : LHLELLVAVGPDVFQ	4 70	21 7	Db.
	KRF _. 213 -RA 75	CGVASG-WNPAILRALDPYKPRRAGFGESRSRRRSGRAKRF	LSPGAPL	AILRALDPY: : : : : SCLQALEPQAVSSY	CGVASG-WNPAILR 	1	17 2	ρ γ
34	Gaps	DB 4; Length 1427; 7e-65; s 347; Indels 151;	re 893.5; I d. No. 5.7e Mismatches	Sco Pre	n Similarity 29.2%; 50; Conservative 1	atcl cal 2	Query M Best Lo Matches	
	PROTEASE.	FACTOR-CLEAVING 1A4442 CRC64;	ENTIAL. WILLEBRAND EB1BC3AABC	POTENTIAL. VON WILLEE 632 MW; EB1BC3	1 33 75 1427 1427 AA; 153	SIGNAL CHAIN SEQUENCE	SIGNAI CHAIN SEQUEI	FT FT

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Search completed: April 29, 2003, 17:17:36 Job time: 66.9303 secs
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Best Local Similarity 54.7%;
Matches 146; Conservative 3
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InterPro; IPR0001590; TSP1.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
SMART; SM00209; TSP1; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50015; ADAM_MEPRO; 1.
PROSITE; PS500142; ZINC_PROTEASE; UNK
PROSITE; PS00142; ZINC_PROTEASE; UNK
NON_TER 269 269
SEQUENCE 269 AA; 29193 MW; 97ALC
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GOAD M.E.;

GOAD D.L., GOAD M.E.;

GOAD D.L., GOAD M.E.;

GOAD D.L., GOAD M.E.;

MOlecular cloning of lapine aggrecanase-2 (ADAMTS-11) from articular chondrocytes.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB317415; AAG33062.1;

HSSP, O9PW35; 1BUD.

HSRDPS; M12, 225; -
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01-MAR-2001 (TrEMBLrel: 16, Last sequence update)
01-JUN-2002 (TrEMBLrel: 21, Last annotation update)
Aggrecanase-2 (Fragment).
ADAMTS-11.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                         SCNLEPCPSSASGKSFREEQCEAFNGY 590
                                                                                                                                                                                                                                                                                                            ----HNLNKHRVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGVRVXYR 563
                                                                                                                                                                                                                                                                        KKKYYSTSSH----GNWGSWGPWGQCSRSCGGGVQFAYRHCNNPAPRNSGRYCTGKRAIYR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELAFGYGSKPCPYMQYCTKLWCTGKAKGQMYCQTRHFPWADGTSCGEGKLCLKGACVER- 507
                                                                                                                                  SCSVTPCP--ANGKSFRHEQCEAKNGY 262
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PS50092; TSP1; 1.
PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Listing first 45 s
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Sequence 352, App
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APPLICANT: Friddle, Carl Johan

APPLICANT: Friddle, Carl Johan

APPLICANT: Hilbun, Erin

TITLE OF INVENTION: No. US20020115842A1el Human Proteases and Polynucleotides Ence

FILE REFERENCE: LEX-0241-USA

CURRENT APPLICATION NUMBER: US/09/965,631

CURRENT FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/236,689

PRIOR APPLICATION NUMBER: US 60/236,689

PRIOR FILING DATE: 2000-09-29

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 950

TYPE: PRT

ORGANISM: homo sapiens

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Best Local Similarity 99.9
Matches 949; Conservative
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US-10-174-579-352

US-10-174-579-352

US-10-174-588-352

US-10-175-740-352

US-10-175-740-352

US-10-176-488-352

US-10-176-492-352

US-10-176-492-352

US-10-176-492-352

US-10-176-492-352

US-10-176-985-352

US-10-176-985-352

US-10-176-987-352

US-10-176-987-352

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; TYPE: PRT
; ORGANISM: HOMO S
US-10-163-316-2
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        Matches
                              Query Match
                                                                                                    SEQ ID NO 2
                                                                                                                                                       APPLICANT: Kapeller-Libermann, Rosana TITLE OF INVENTION: 65552, A Human Matrix TITLE OF INVENTION: Therefor FILE REFERENCE: MPIO1-025PLRNM CURRENT APPLICATION NUMBER: US/10/163,316 CURRENT FILING DATE: 2002-06-05
                                                                                                            PRIOR APPLICATION NUMBER: 60/297,
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Vei
Local ... 791;
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                 Similarity
        Conservative
                  82.2%;
96.9%;
      Score 4242.5;
Pred. No. 5.56
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CURRENT APPLICATION NUMBER: US/09/321, CURRENT FILING DATE: 1999-05-28 PRIOR APPLICATION NUMBER: 60/087,170 PRIOR FILING DATE: 1998-05-29 PRIOR APPLICATION NUMBER: 60/129,023 PRIOR FILING DATE: 1999-04-13 NUMBER OF SEQ ID NOS: 5
                                                                                           APPLICANT: Blelloch, Robert H
TITLE OF INVENTION: Agent and Method
FILE REFERENCE: 960296.95386
                                                                                                                        APPLICANT: Kimble, APPLICANT: Blello
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Best Local :
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SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 LLLLASITMLLCARGAHGRPTEEDEELVLP-SLE-----RAPGHDSTTTRL--RL
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GHEVVSAVERDLVVKGSLLRYSGTGTAVESLQASRPILEPLTVEVLSVGKMTPPRVRYSF 798
                                                                                                                                                                                                NKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLN 738
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                                             FMKKKTES-----FNAIPTFS-----EWVIEEWGECSKTCGSG
                                                                        YLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWGPCSASCGSG
                                                                                                      GNETLSTLEQDLTYKGTVLRYSGSSAALERIRSESPLKEPLTIQVLMVGHALRPKIKETY
                                                                                                                                                                  GSTCKKMSGIVTSTRPGYHDIVTIPAGATNIEVKHRNQRGSRNNGSFLAIRAADGTYILN
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48.0%; Pred. No. 4e-169
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; LENGTH: 968
; TYPE: PRT
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Matches 478
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Publication No. US20020197703A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kapeller-Libermann, Rosana
TITLE OF INVENTION: 65552, A Human Matrix Metalloproteinase
TITLE OF INVENTION: Therefor
FILE REFERENCE: MPTO1-02591RNM
CURRENT APPLICATION NUMBER: US/10/163,316
CURRENT FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/297,863
PRIOR APPLICATION NUMBER: 60/297,863
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 10
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                                                                                       ----SGRAKREVSIPRYVETLVVADESMVKFHGADLEHYLLTLLATAARLYRHPSILNPI 262
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 RVKYRSCNLEPCPSSASGKSFREEQCEAFNGYNHSTNRLTLAVAWVPKYSGVSPRDKCKL 618
                                 GKCVNKTDM-KHFATPVHGSWGPWGPWGDCSRTCGGGVQYTMRECDNPVPKNGGKYCEGK
                                                 GACVERHNINKH---RVDGSWAKWDPYGPCSRTCGGGVQLARRQCTNPTPANGGKYCEGV 558
                                                                                                                                                                                                                                                                              SLVVVKILVIYEEQKGPEVTSNAALTLRNFCNWQKQHNSPSDRDPEHYDTAILFTRQDLC
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48.0%; pred. No. 4.1e-169;
tive 158; Mismatches 249;
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APPLICANT: GOODERI, AND TANGO-73, TANGO-74, TANGO-76, AND TITLE OF INVENTION: TANGO-71, TANGO-73, TANGO-74, TANGO-76, AND FILE REFERENCE: 09404/041001

CURRENT APPLICATION NUMBER: US/10/105,929

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/130,49

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/058

PRIOR FILING DATE: EARLIER APPLICATION NUMBER: US 60/058

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/058

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/054

PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-06

NUMBER OF SEQ ID NOS: 16

SOFTMARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo
US-10-105-929-2
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US-10-105-929-2
; Sequence 2, A
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Best Local
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                                                                                                                                                                                                                                                                     LLLLAAALLAVSDALGRPSEEDEELVVP-ELE-----RAP---GHGTTRLRLHAF
                                                                                                                              AAVSLCGGLRGAFGYRGAEYVISPLPNAS---APAAQRNSQGA----HLLQ--RRGVPGG 165
                                                                                                                                                                                     DQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLP----ETDLAHCFYSGTVNGDPSSA 136
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18; Pred. No. 5.7e-169;
154; Mismatches 251;
                                                             ---GVASG--WNPAILRALDPYKPRRAGFGESRSRRRS
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APPLICANT: Hirose,
APPLICANT: Inoguch
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APPLICANT:
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FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/10/097,597
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
                                                                                                   APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein,
TITLE OF INVENTION: pharmaceutical
TITLE OF INVENTION: composition and method
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Hakozaki, Michinori
Ishioka, Keiko
Ishida, Yukako
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RESULT 7
US-10-097-580-1
Sequence 1, Application US/10097580
Publication No. US20030032168A1
GENERAL INFORMATION:
APPLICANT: Hirose, Kunitaka
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PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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Best Local Similarity
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TYPE: PRT
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APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
TITLE OF INVENTION: Human ADAMTS-1 protein, ger
TITLE OF INVENTION: composition and method of
FILE REFERENCE: Q57092
CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR APPLICATION NUMBER: JS 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS! 14
SEQ ID NO 1
LENGTH: 727
TYPEF: PRT
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Hakozaki, Michinori
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Ishida, Yukako
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54.4%; Pred. No. 2
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US-09-445-023A-1
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PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
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Best Local Similarity
Matches 408; Conserv
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CURRENT APPLICATION NUMBER: US/09/445,023A
CURRENT FILING DATE: 1999-12-03
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                                   VTGLFTKPMHGYNEVVAIPAGASSIDIRQRGYKGLIGDDNYLALKNSQGKYLLNGHFVVS 744
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Ishida, Yukako
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Best Local Similarity
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CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
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PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
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                                                                                                                       QFTFGEESKHCPDAASTCTTLWCTGTSGGLLVCQTKHFPWADGTSCGEGKWCVSGKCVNK
                                                                   ELAFGYGSKPCP-YMQYCTKLWCTGKAKGQMYCQTRHFPWADGTSCGEGKLCLKGACVER
                                                                                                      {\tt LMASMLSSLDHSQPWSPCSAYMVTSFLDNGHGECLMDKPQNPIKLPSDLPGTLYDANRQC}
                                                                                                                                                                             TLGMADVGTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDDAKHCASLNGVSGDSH
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Kuno, Kouji
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Ishida, Yukako
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Hakozaki, Michinori
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53.7%;
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Pred. No. 2.6e-154;
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RESULT 10
US-10-097-580-12
; Sequence 12, Application US/10097580
; Publication No. US20030032168A1
; GENERAL INFORMATION:
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US-10-097-580-12
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                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/097,580
CURRENT FILLING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 09/445,023
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: JP 9-160422
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Human ADAMTS-1 protein, TITLE OF INVENTION: composition and method FILE REFERENCE: 057092
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APPLICANT: Hakozaki, Michinori
APPLICANT: Ishida, Keiko
APPLICANT: Ishida, Yukako
APPLICANT: Matsushima, Kouji
APPLICANT: Kuno, Kouji
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                                                                                                                                           403;
                                                                                                                                         Conservative
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Pred. No. 2.6e-154;
ll; Mismatches 176;
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; LENGTH: 727
; TYPE: PRT
; ORGANISM: Mus s
US-09-445-023A-12
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                                                                SEQ ID NO 12
                                                                                                                                                                                                                                      APPLICANT:
                                                                          CURRENT APPLICATION NUMBER: US/09/445,023A CURRENT FILING DATE: 1999-12-03 PRIOR APPLICATION NUMBER: JP 9-160422 PRIOR FILING DATE: 1997-06-03 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin version 3.0
                                                                                                                                                                         TITLE OF INVENTION: Human ADAMTS-1 protein, TITLE OF INVENTION: composition and method FILE REFERENCE: Q57092
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Hakozaki, Michinori
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Query Match

44.0%;

Score

2273;

DB

10;

Length

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RESULT 12
US-09-918-171A-9
CURRENT APPLICATION NUMBER: US/09/918,171A CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: 09/369,364 PRIOR FILING DATE: 1999-08-06 NUMBER OF SEQ ID NOS: 31 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 9
                                                                                                                                                                     Sequence 9, Application US/09918171A Patent No. US20020110894A1 GENERAL INFORMATION:
                                                                                               APPLICANT: Apte, Suneel
APPLICANT: Hurskainen, Tiina L.
APPLICANT: Hirohata, Satoshi
TITLE OF INVENTION: Nucleic Acids
FILE REFERENCE: 26473/04193
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403; Conservative 131;
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                                                                                              TPPRVRYSFYLPKEPREDKSSHPKDPRGPSVLHNSVLSLSNQVEQPDDRPPARWVAGSWG
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              ECPSTCRGSWQRRTVECRDPSGQAS-DTCDEALKPEDAKPCGSQPCP
                                                                                                                                                                                    KCGVCGGKGTACRKISGSFTPFSYGYNDIVTIPAGATNIDVKQRSHPGVRNDGSYLALKT
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                                       PCSASCGSGLQKRAVDCRGSAGQRTVPACDAAHRPVETQACG-EPCP
                                                                   FPPKVRYTFFVPND--MDFSVQNSKERATT---NIIQSL-
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Pred. No. 9.5e-143;
8; Mismatches 260;
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CURRENT APPLICATION NUMBER: US/09/972,467
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID MOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1629
TYPE: PRT
ORGANISM: Human
US-09-972-467-2
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APPLICANT: PPIZER INC.
TITLE OF INVENTION: ADAMTS POLYPEPTIDES, NUCLEIC ACIDS ENCODING THEM, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: PC10850A
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Best Local Similarity 39.9%; Pred. No. 7.7e
Matches 411; Conservative 145; Mismatches
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                                 GNTAYYQLRDRVIDGTPCGQDTNDICVQGLCRQAGCDHVLNSKARRDKCGVCGGDNSSCK 753
                                                     GTGYFYVLAPKVVDGTLCSPDSTSVCVQGKCIKAGCDGNLGSKKRFDKCGVCGGDNKSCK 683
                                                                                              SCNTEPCLKQK--RDFRDEQCAHEDGKHENINGLLPNVRWVFKYSGILMKDRCKLFCRVA 693
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	Qy 121 GG-LRGAFGYRGAEYVISPLPNASAPAAQRNSQGAHLLQRRGVPGGPSGDPTSRCGVASG 179	
	Qy 61 QEDEYLHLTPDAQFLAPAFSTEHLGVPLQGLTGGSSDLRRCFYSGDVNAEPDSFAAVSLC 120	п о
	Qy 1 MLLLGILTLAFAGRTAGGFEPEREVVVPIRLDPDINGRRYYWRGPEDSGDQGLIFQITAF 60 :	по
16;	Query Match 37.1%; Score 1916; DB 9; Length 837; Best Local Similarity 46.3%; Pred. No. le-128; Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps	
	TYPORG	a
	TETLING DATE: 2002-06-18	
	TITLE OF INVENTION: SECTOR ENCODING THE SAME	
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	APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian	·. ·.
	NO. US20030008352A1	
	352 Application III	· C ઋ
	b 1045 IQRCSEFPC 1053	Db
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	986 PSNREKCSGECNTGGWRYSAWTECSKSCDGGTQRRRAICVNTRNDVLDDSKCT-HQEKVT 1044	Db
	884	Qy
	926 HITEPCGTDCDLRWHVASRSECSAQ	da
	y 841ARWVAGSWGPCSASCGSGLQKRAVDCRGSAGQRTVPACDAAHR 883	Qy
	B74 DKPQQFYWNSHGPWQACSKPCQGERKRKLVCTRESDQLTVSDQRCDRLPQPG 925	ДD
	804 PREDKSSHPKDPRGPSVLHNSVLSLSNQV	Qy
•	b 814 TMAKREIRIGNAVVEYSGSETAVERINSTDRIEQELLLQVLSVGKLYNPDVRYSFNIPIE 873	ДĎ
	744	Qy
	Db 754 TVAGTENTVHYGYNTVVRIPAGATNIDVRQHSESGETDDDNYLALSSSKGEELLNGNEVV 813	D

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                                                                                                              Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 352
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APPLICANT: Baker, Ke
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  Matches
                             Query Match
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APPLICANT:
APPLICANT:
                                                                                                                                                                                   APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
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CURRENT FILING DATE: 2002-06-21
                                                                                   LENGTH: 837
TYPE: PRT
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 381;
             Similarity
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                                                                           QRGYKGLIGDDNYLALKNSQGKYLLNGHFVVSAVERDLVVKGSL-LRYSGTGTAVESLQA
                                                                                                            RCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFRKFRYGYNNVVTIPAGATHILVR
                                                                                                                                    KCIKAGCDGNLGSKKRFDKCGVCGGDNKSCKKVTGLFTKPMHGYNFVVAIPAGASSIDIR
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                          SRPILEPLTVEVLSVGKMTPPRVRYSFYLPKEPREDKSSHPKD
                                                           QQGNPG--HRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGAVSLRYSGATAASETLSG
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                                                                                                                                                                                                                                          VQFSSRDCTRPVPRNGGKYCEGRRTRFRSCNTEDCP-TGSALTFREEQCAA---YNHRTD
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Job time: 32.1175 secs